

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 26, 2004, 16:59:06 ; Search time 12,1928 Seconds
(without alignments)
1996.498 Million cell updates/sec

Title: US-10-655-873-8
Perfect score: 1304
Sequence: 1 MWPPGSASQPPPPSPAAATGL.....HAFRIRAVTIDRVMSYLNAS 253

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1304	100.0	253	2 B38957	interleukin 12A pr
2	644	49.4	215	2 I56135	interleukin 12 p35
3	98.5	7.6	438	2 T45785	hypothetical prote
4	97	7.4	1301	2 T07321	DNA-directed RNA p
5	93.5	7.2	1489	2 G83771	hypothetical prote
6	91	7.0	661	2 T08872	hypothetical prote
7	91	7.0	729	1 A34796	kinesin-related,pr
8	90.5	6.9	781	1 TVFFDF	protein kinase Dra
9	90	6.9	349	2 D70398	hypothetical prote
10	89.5	6.9	680	2 T04647	hypothetical prote
11	89.5	6.9	1040	2 AH1926	hypothetical prote
12	89	6.8	586	2 JC4778	pectinesterase (EC
13	88.5	6.8	1111	2 T01078	hypothetical prote
14	87	6.7	1445	2 T50508	hypothetical prote
15	86	6.6	407	2 F72343	hypothetical prote
16	86	6.6	830	1 B44047	glycoprotein B pre
17	86	6.6	830	2 T44186	probable glycoprot
18	86	6.6	830	2 T43999	glycoprotein B [im
19	85.5	6.6	868	2 T25716	hypothetical prote
20	85.5	6.6	950	2 T38777	probable valyl trn
21	85.5	6.6	1121	2 T25715	hypothetical prote
22	85	6.5	930	2 T32017	hypothetical prote
23	85	6.5	4385	2 T29042	hypothetical prote
24	84	6.4	3968	2 A44265	trithorax homolog
25	83.5	6.4	630	2 A49656	estrogen-responsiv
26	83.5	6.4	816	2 D84601	hypothetical prote
27	83	6.4	287	2 T48548	hypothetical prote
28	83	6.4	830	1 A44047	glycoprotein B pre
29	83	6.4	1698	2 S51869	probable membrane

30	82.5	6.3	460	2 B48057	farnesyl-diphospha
31	82.5	6.3	460	2 T40581	farnesyl-diphospha
32	82.5	6.3	583	2 S01496	lamin B - African
33	82.5	6.3	817	2 S53921	hypothetical prote
34	82	6.3	508	1 KRSHL2	keratin type II, m
35	82	6.3	542	2 T19925	hypothetical prote
36	82	6.3	554	2 T51213	hypothetical prote
37	82	6.3	808	2 A96791	hypothetical prote
38	82	6.3	958	2 T20621	hypothetical prote
39	82	6.3	1094	2 S22573	DNA-directed DNA p
40	81.5	6.2	542	2 A82965	hypothetical prote
41	81.5	6.2	561	2 T07649	hypothetical prote
42	81.5	6.2	603	2 T16655	hypothetical prote
43	81.5	6.2	873	2 H85134	polyubiquitin-like
44	81.5	6.2	3092	2 S46009	Gtpase-activating
45	81	6.2	576	2 T48573	hypothetical prote

ALIGNMENTS

RESULT 1

B38957

interleukin 12A precursor [validated] - human

N;Alternate names: cytotoxic lymphocyte maturation factor 35K chain; natural killer cel
C;Species: Homo sapiens (man)

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C;Accession: B38957; A39359; A36055

R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.;
i, G.; Perussia, B.

J. Immunol. 146, 3074-3081, 1991

A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric cy
A;Reference number: A38957; MUID:91201875; PMID:1673147

A;Accession: B38957

A;Molecule type: mRNA

A;Residues: 1-253 <WOL>

A;Cross-references: UNIPROT:O60595; GB:M65290

A;Note: it is uncertain whether Met-1 or Met-35 is the initiator

R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nabav
Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991

A;Title: Coexpression of two distinct genes is required to generate secreted bioactive
A;Reference number: A39359; MUID:91239523; PMID:1674604

A;Accession: A39359

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 35-246, 'T', 248-253 <GUB>

A;Cross-references: GB:M65271; GB:M38443; NID:g180623; PIDN:AAA35694.1; PID:g180624

R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.;
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990

A;Title: Purification to homogeneity and partial characterization of cytotoxic lymphocy
A;Reference number: A36055; MUID:90370873; PMID:2204066

A;Accession: A36055

A;Status: preliminary

A;Molecule type: protein

A;Residues: 'X', 58-70, 'X', 72-82 <STE>

C;Genetics:

A;Gene: GDB:IL12A; NKSF1

A;Cross-references: GDB:127869; OMIM:161560

A;Map position: 3p12-3q13.2

C;Keywords: cytokine; glycoprotein; heterodimer

F;57-253/Product: interleukin 12A #status predicted <MAT>

F;127,141,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1304; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.5e-101;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWPPGSASQPPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLVATLVLLDHLSLARNLP 60

|||||
1 MWPPGSASQPPPPSPAAATGLHPAARPVSLQCRLSMCPARSLLLVATLVLLDHLSLARNLP 60

Qy 61 VATPDGFMFPCLHHSQNLIRAVSNMLQKARQTLFYPCTSEIDHEDITKDKTSTVEACL 120
|||||

Db 61 VATPDGMPFCLHHSQNLRAVSNMLQKARQTLFYPCTSEEDHEDITKDKTSTVEACL 120
Qy 121 PLELTKNESCLNSRETSTFINGSCLSARKTSMFALCLSSIEDLKMYQVEFKTMNAKLL 180
Db 121 PLELTKNESCLNSRETSTFINGSCLSARKTSMFALCLSSIEDLKMYQVEFKTMNAKLL 180
Qy 181 MDPKQIFLDQNLAVIDELMQALNFNSETVPQKSSLEEDFYKTKIKLCILHAFRIRA 240
Db 181 MDPKQIFLDQNLAVIDELMQALNFNSETVPQKSSLEEDFYKTKIKLCILHAFRIRA 240
Qy 241 VTIDRVMSYLNAS 253
Db 241 VTIDRVMSYLNAS 253

RESULT 2
I56135
interleukin 12 p35 subunit - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I56135
R;Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K.;
J. Immunol. 148, 3433-3440, 1992
A;Title: Cloning and Expression of Murine IL-12.
A;Reference number: I56135; MUID:92268481; PMID:1350290
A;Accession: I56135
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: UNIPROT:P43431; GB:M86672; NID:g198336; PIDN:AAA39292.1; PID:g198337

Query Match 49.4%; Score 644; DB 2; Length 215;
Best Local Similarity 58.9%; Pred. No. 2.5e-46;
Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;

Qy 35 MCPARSLLLVATLVLLDHLHSLARNLPVATPDGMPFCLHHSQNLRAVSNMLQKARQTL 94
Db 1 MCQSYLLFLATLALNLHLSLARVIPVSGP---ARCLSQSRNLLKTDDMVKTAREKLL 56

Qy 95 FYPCTSEEDHEDITKDKTSTVEACLPLELTKNESCLNSRETSTFINGSCLSARKTSPMM 154
Db 57 HYSCTAEDIDHEDITRDQTSILKTCPLPLELHKNESCLATFETSTTRGSCLPPOKTSLMM 116

Qy 155 ALCLSSIEDLKMYQVEFKTMNAKLLMDPKQIFLDQNLAVIDELMQALNFNSETVPQK 214
Db 117 TLCGLSIEDLKMYQTEFOAINALQNHNHQIILDKGLVAIDELMQSLNHNGETLRQK 176

Qy 215 SSLEEDFYKTKIKLCILHAFRIRAATIDRVMSYLNAS 253
Db 177 PVPGEADPYRVKMKLCILHAFSTRVVTINRVMGYLSSA 215

RESULT 3
T45785
hypothetical protein F26O13.180 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45785
R;Delseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23013
A;Accession: T45785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-438
A;Cross-references: UNIPROT:Q9SC25; EMBL:AL133452
A;Experimental source: cultivar Columbia; BAC clone F26O13
C;Genetics:
A;Map position: 3
A;Introns: 35/1; 67/2; 104/3; 326/3
A;Note: F26O13.180

Query Match 7.6%; Score 98.5; DB 2; Length 438;

Best Local Similarity 25.6%; Pred. No. 1.5;
Matches 42; Conservative 27; Mismatches 48; Indels 47; Gaps 9;

Qy 3 PPGSASQPPSPAAATGLHPAARPVSLQCRLSMC---PARSLLVATLVLLDHLHSLARN 58
Db 272 PKGRSASPSLIPTFSGTSHTTTPKSIKPSATVADSTRPGKLSRASVQMAINHLDLARN 331

Qy 59 LPVAT---PDPGMFPCILHHSQNLRAVSNMLQKARQTLFYPCTSEEDHEDH 105
Db 332 GKVSTHTTFSSPMLYP---HS---IRSSSSGLRK-----PCGSSEGCSSSSNHEEDG 377

Qy 106 EDITKDKTSTVEACLPLELTKNESC-----LN---SRETSPITN 141
Db 378 RSLTKEGNTE-----NKNDARYDALLNVKDVKDTNWLNL 413

RESULT 4
T07321
DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Chlorella vulgaris chloroplast
C;Species: chloroplast Chlorella vulgaris
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07321
R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Taudzuki, J.; Naka
Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997
A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chl
A;Reference number: Z15985; MUID:97303241; PMID:9159184
A;Accession: T07321
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1301 <WAK>
A;Cross-references: UNIPROT:P56299; EMBL:AB001684; NID:g2224352; PIDN:BAA57969.1; PID:g
C;Genetics:
A;Gene: rpoB
A;Genome: chloroplast
C;Superfamily: DNA-directed RNA polymerase beta chain
C;Keywords: chloroplast; nucleotidyltransferase

Query Match 7.4%; Score 97; DB 2; Length 1301;
Best Local Similarity 22.4%; Pred. No. 7.8;
Matches 54; Conservative 33; Mismatches 92; Indels 62; Gaps 10;

Qy 44 VATLVLLDHLHSLARNLPVATPDGMPFCLHHSQ-NLLRAVSNMLQKARQTL----- 94
Db 574 VATRITTSQVGILQNISVAT---SLIPFLEHNDANRALMGSNMORQAVPLLKQAPLVGT 630

Qy 95 -FYPCTSEEDHEDITKDKTSTVEACL-----DITKDKTSTVEACL-----LELTKNESC 130
Db 631 GLESRVIGDVNHSMQASKTGFTTKVSSTKIQVLSPRKTKAQSVMFSLNKKKKSL 690

Qy 131 LNSRETSTFINGSC-----ASRKTSMFALCLSSIEDLKMYQVEFKTMNAKLLMDP 183
Db 691 LNSEKQSFSGKNGIFFIKTLQKSNLKNIFFSA--QKALYQENSFSLKFEAQNR--LFIP 746

Qy 184 KRQIFLDQNLAVIDELMQALNFNSETV--PQK-----SSLEEDFYKTKIK 228
Db 747 KMTFSLAQNFSTRKIPFLSFFLKKKKERPRNPKKFFRSDSFVNMKHKLHSEDFRKNKVE 806

Qy 229 L 229
Db 807 I 807

RESULT 5
G83771
hypothetical protein BH0975 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83771
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83771

KW Human; interleukin 12; IL-12; heterodimeric complex; immunogenic;
KW Leishmania; antigen; leishmaniasis; cell-mediated immunity; adjuvant;
KW TH1 helper cell; TH2 helper cell; alum; cytokine; bacterium; cancer;
KW vaccine; cell surface; membrane; glycoprotein; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US5571515-A.
XX
PD 05-NOV-1996.
XX
PF 17-JUN-1994; 94US-00265087.
XX
XX 18-APR-1994; 94US-00229282.
PR
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Trinchieri G, Scott P;
XX
DR WPI; 1996-505347/50.
DR N-PSDB; AAT48098.
XX
XX Immunogenic compsn. to improve cell mediated immune response - contains
PT soluble leishmania antigen and interleukin-12 as adjuvant.
PT
XX Disclosure; Col 17-22; 22pp; English.
PS
XX This is the amino acid sequence of the human interleukin (IL)-12 40 kD
CC subunit. IL-12 is a heterodimeric complex composed of the 40 kD subunit
CC and a 30 kD subunit (AAW07399). The complex is used in a novel
CC immunogenic composition comprising a soluble Leishmania antigen with IL-
CC 12, for protection against leishmaniasis. The addition of IL-12 improves
CC cell-mediated immunity by inducing TH1 helper cells (as opposed to TH2
CC cells which are induced by alum adjuvant) and does not cause uncontrolled
CC release of other cytokines (in contrast to bacterial adjuvants). IL-12
CC can also be used as a cancer vaccine by association with the protein B7,
CC a soluble, cell-surface (membrane)-bound glycoprotein which is expressed
CC in antigen presenting cells. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 328 AA;

Query Match 100.0%; Score 1758; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.5e-148;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCHQQLVISWFSVLFLASPLVAIWELKDDVYVVELDWYDPAPGEMVVLTCDTPEEDGITW 60
Db 1 MCHQQLVISWFSVLFLASPLVAIWELKDDVYVVELDWYDPAPGEMVVLTCDTPEEDGITW 60
QY 61 TLDQSSEVLGSGKTLTIQVKEFGDAGQYTCCHKGGEVLSHSLLLHKKEDGIWSTDILKDQ 120
Db 61 TLDQSSEVLGSGKTLTIQVKEFGDAGQYTCCHKGGEVLSHSLLLHKKEDGIWSTDILKDQ 120
QY 121 KEPKNTFLRCEAKNYSGRFTCWLTITISTDLTSPSVKSSRGSSDPQGVTCGAATLSAERV 180
Db 121 KEPKNTFLRCEAKNYSGRFTCWLTITISTDLTSPSVKSSRGSSDPQGVTCGAATLSAERV 180
QY 181 RGDNKEYEYSEVCEQDSACPAEESLPVEMVDVAVHKLKYENYTSFFIRDIKPDPPKN 240
Db 181 RGDNKEYEYSEVCEQDSACPAEESLPVEMVDVAVHKLKYENYTSFFIRDIKPDPPKN 240
QY 241 LQKPLKNSRQVEVSWEYPTWTSTPHSYFSLTFCVQVQGSKRKKDRVFTDKTSATVIC 300
Db 241 LQKPLKNSRQVEVSWEYPTWTSTPHSYFSLTFCVQVQGSKRKKDRVFTDKTSATVIC 300
QY 301 RKNASISVRAQDRYSSSWSEWASVPCS 328
Db 301 RKNASISVRAQDRYSSSWSEWASVPCS 328

AAW24235
ID AAW24235 standard; protein; 328 AA.
XX
AC AAW24235;
XX
DT 25-MAR-2003 (revised)
DT 18-MAR-1998 (first entry)
XX
DE 40 kDa subunit of human cytotoxic lymphocyte maturation factor.
XX
KW Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;
KW interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;
KW CLMF bioactivity inhibition; affinity ligand; transplacental;
KW cytotoxic T cell proliferation.
XX
OS Homo sapiens.
XX
PN EP790255-A2.
XX
PD 20-AUG-1997.
XX
PF 09-DEC-1990; 97EP-00104656.
XX
PR 22-DEC-1989; 89US-00455708.
PR 09-MAY-1990; 90US-00520935.
PR 27-AUG-1990; 90US-00572284.
PR 09-DEC-1990; 90EP-00123670.
XX
(HOFF) HOFFMANN LA ROCHE & CO AG P.
PI Chizzonite RA, Gately MK, Gubler UA, Hulmes JD, Pan YE;
PI Podlanski FJ, Stern AS;
XX
DR WPI; 1997-404698/38.
DR N-PSDB; AAT77849.
XX
PT Antibodies to cytotoxic lymphocyte maturation factor protein - useful as
PT affinity ligands, assay reagents and medicaments.
XX
PS Claim 2; Fig 25; 80pp; English.
XX
CC The present sequence represents the 40 kDa subunit of cytotoxic
CC lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
CC a 75 kDa heterodimer, where the 2 subunits (see AAW24236 for the 35 kDa
CC subunit) are bonded together via one or more disulphide bonds. CLMF
CC protein is produced by a human B lymphoblastoid cell line. CLMF
CC synergistically induces, in the presence of interleukin-2, the cytolytic
CC activity of lymphokine activated killer cells. CLMF is also capable of
CC stimulating T-cell growth. A novel antibody directed against an epitope
CC of CLMF protein (see AAW24237 for epitope) is capable of neutralising
CC and/or inhibiting CLMF bioactivity. This antibody may be used as an
CC affinity ligand for purifying the CLMF protein. The antibody can also be
CC used as an assay reagent for detecting the CLMF protein, and as a
CC medicament for selectively blocking the proliferation and activation of
CC cytotoxic T cells, e.g. in transplantation. (Updated on 25-MAR-2003 to
CC correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 328 AA;

Query Match 100.0%; Score 1758; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.5e-148;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCHQQLVISWFSVLFLASPLVAIWELKDDVYVVELDWYDPAPGEMVVLTCDTPEEDGITW 60
Db 1 MCHQQLVISWFSVLFLASPLVAIWELKDDVYVVELDWYDPAPGEMVVLTCDTPEEDGITW 60
QY 61 TLDQSSEVLGSGKTLTIQVKEFGDAGQYTCCHKGGEVLSHSLLLHKKEDGIWSTDILKDQ 120
Db 61 TLDQSSEVLGSGKTLTIQVKEFGDAGQYTCCHKGGEVLSHSLLLHKKEDGIWSTDILKDQ 120
QY 121 KEPKNTFLRCEAKNYSGRFTCWLTITISTDLTSPSVKSSRGSSDPQGVTCGAATLSAERV 180
Db 121 KEPKNTFLRCEAKNYSGRFTCWLTITISTDLTSPSVKSSRGSSDPQGVTCGAATLSAERV 180

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 26, 2004, 09:32:55 ; Search time 437.322 Seconds
(without alignments)
15189.855 Million cell updates/sec

Title: US-10-655-873-11
Perfect score: 1193
Sequence: 1 tgaagatcagctattagaag.....taaagtgaagttcacaact 1193

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1193	100.0	1193	15	US-10-284-740-13
2	1193	100.0	1193	16	US-10-641-643-1302
3	1193	100.0	1193	17	US-10-283-975A-258
4	1193	100.0	1193	17	US-10-654-796-6
5	1193	100.0	1193	17	US-10-654-763-6
6	1193	100.0	1193	18	US-10-733-878-280
7	963.2	80.7	987	10	US-09-882-945A-141
8	963.2	80.7	987	18	US-10-807-114-141
9	718.8	60.3	5961	15	US-10-429-802-35
10	718.8	60.3	5961	16	US-10-430-503-26
11	501.8	42.1	601	15	US-10-267-384-168
12	499.4	41.9	501	16	US-10-411-037-19
					Sequence 13, Appl
					Sequence 1302, Ap
					Sequence 258, App
					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 280, App
					Sequence 141, App
					Sequence 141, App
					Sequence 35, Appl
					Sequence 26, Appl
					Sequence 168, App
					Sequence 19, Appl

13	499.4	41.9	501	16	US-10-411-026-19	Sequence 19, Appl
14	499.4	41.9	501	16	US-10-410-962-19	Sequence 19, Appl
15	499.4	41.9	501	16	US-10-411-049-19	Sequence 19, Appl
16	499.4	41.9	501	17	US-10-410-930-19	Sequence 19, Appl
17	499.4	41.9	501	17	US-10-410-997-19	Sequence 19, Appl
18	499.4	41.9	501	17	US-10-411-012-19	Sequence 19, Appl
19	499.4	41.9	501	17	US-10-287-994-19	Sequence 19, Appl
20	499.4	41.9	501	17	US-10-410-913-19	Sequence 19, Appl
21	499.4	41.9	501	18	US-10-276-642-1	Sequence 1, Appli
22	496.4	41.6	498	17	US-10-432-777-13	Sequence 13, Appl
23	433.2	36.3	438	15	US-10-151-469-22	Sequence 22, Appl
24	433.2	36.3	438	16	US-10-422-523-17	Sequence 17, Appl
25	347	29.1	567	15	US-10-151-469-21	Sequence 21, Appl
26	347	29.1	567	16	US-10-422-523-16	Sequence 16, Appl
27	347	29.1	583	15	US-10-205-534-9	Sequence 9, Appli
28	347	29.1	623	15	US-10-205-534-7	Sequence 7, Appli
29	325.2	27.3	538	15	US-10-151-469-20	Sequence 20, Appl
30	325.2	27.3	538	16	US-10-422-523-15	Sequence 15, Appl
31	306	25.6	498	13	US-10-116-273-42	Sequence 42, Appl
32	306	25.6	498	15	US-10-195-707B-42	Sequence 42, Appl
33	306	25.6	498	15	US-10-186-962-5	Sequence 5, Appli
34	282.2	23.7	375	15	US-10-369-495-3	Sequence 3, Appli
35	245.6	20.6	368	16	US-10-131-827-8202	Sequence 8202, Ap
36	222.6	18.7	322	16	US-10-131-827-8477	Sequence 8477, Ap
C 37	213	17.9	514	16	US-10-131-827-8745	Sequence 8745, Ap
C 38	191.6	16.1	576	16	US-10-131-827-8181	Sequence 8181, Ap
C 39	185.2	15.5	594	16	US-10-131-827-8744	Sequence 8744, Ap
C 40	185	15.5	185	9	US-09-864-761-19121	Sequence 19121, A
C 41	181.6	15.2	480	9	US-09-864-761-2388	Sequence 2388, Ap
42	172.2	14.4	308	15	US-10-279-061-71	Sequence 71, Appl
43	172.2	14.4	309	15	US-10-279-061-81	Sequence 81, Appl
44	172.2	14.4	393	15	US-10-279-061-87	Sequence 87, Appl
45	169.8	14.2	370	16	US-10-131-827-8700	Sequence 8700, Ap

ALIGNMENTS

RESULT 1

US-10-284-740-13
; Sequence 13, Application US/10284740
; Publication No. US20030138404A1
; GENERAL INFORMATION:
; APPLICANT: Maroun, Leonard E.
; TITLE OF INVENTION: INTERFERON ANTAGONISTS USEFUL FOR THE TREATMENT OF INTERFERON RE
; DISEASES
; FILE REFERENCE: 18448/2002
; CURRENT APPLICATION NUMBER: US/10/284,740
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 09/845,260
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/067,398
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: US 08/502,519
; PRIOR FILING DATE: 1995-07-14
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(609)
; OTHER INFORMATION:
US-10-284-740-13

Query Match 100.0%; Score 1193; DB 15; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2.6e-244;
Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TGAAGATCAGCTATTAGAAGAGAAGATCAGTTAAGTCCTTTGGACCTGATCAGCTTGAT 60
|||||

Db 1 TGAAGATCAGCTATTAGAAGAGAAAGATCAGTTAAGTCCTTTGGACCTTGATCAGCTTGAT 60

Qy 61 ACAAGAACTACTGATTTCAACTCTTTGGCTTAATTTCTCTCGGAAACGATGAAATATACA 120

Db 61 ACAAGAACTACTGATTTCAACTCTTTGGCTTAATTTCTCTCGGAAACGATGAAATATACA 120

Qy 121 AGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTGGGTTCTCTTGGCTGTACTGCCAG 180

Db 121 AGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTGGGTTCTCTTGGCTGTACTGCCAG 180

Qy 181 GACCCATATGTAAGAAGCAGAAAAACCTTAAGAAATATTTTAATGCAGTCAATTCAGAT 240

Db 181 GACCCATATGTAAGAAGCAGAAAAACCTTAAGAAATATTTTAATGCAGTCAATTCAGAT 240

Qy 241 GTAGCGGATAATGGAACCTCTTTCTTAGGCATTTTGAAGAATTTGGAAGAGGAGAGTGAC 300

Db 241 GTAGCGGATAATGGAACCTCTTTCTTAGGCATTTTGAAGAATTTGGAAGAGGAGAGTGAC 300

Qy 301 AGAAAAATAATGCAGAGCCAAATTGTCCTCTTTTACTTCAAACTTTTAAAAAATTAAA 360

Db 301 AGAAAAATAATGCAGAGCCAAATTGTCCTCTTTTACTTCAAACTTTTAAAAAATTAAA 360

Qy 361 GATGACCAGAGCATCCAAAAGAGTGTGGAGACCATCAAGGAAGACATGAATGTCAAGTTT 420

Db 361 GATGACCAGAGCATCCAAAAGAGTGTGGAGACCATCAAGGAAGACATGAATGTCAAGTTT 420

Qy 421 TTCAATAGCAACAAAAAGAAACGAGATGACTTCGAAAAAGCTGACTAATTAATTCGGTAAT 480

Db 421 TTCAATAGCAACAAAAAGAAACGAGATGACTTCGAAAAAGCTGACTAATTAATTCGGTAAT 480

Qy 481 GACTTGAATGTCCAAACGCAAGCAATACATGAATCATCCAAAGTGTGCTGAACTGTGCG 540

Db 481 GACTTGAATGTCCAAACGCAAGCAATACATGAATCATCCAAAGTGTGCTGAACTGTGCG 540

Qy 541 CCAGCAGCTAAACAGGGAAGCGAAAAAGGAGTCAAGTGTGCTGTTTCAAGTTCGAAGACA 600

Db 541 CCAGCAGCTAAACAGGGAAGCGAAAAAGGAGTCAAGTGTGCTGTTTCAAGTTCGAAGACA 600

Qy 601 TCCCAGTAATGGTGTCTGCTGCTGCAATATTTGAATTTTAAATCTAAATCTATTATTAA 660

Db 601 TCCCAGTAATGGTGTCTGCTGCTGCAATATTTGAATTTTAAATCTAAATCTATTATTAA 660

Qy 661 TATTTAACATTATTTATATGCGGAATATATTTTAGACTCATCAATCAATAAAGTATTTA 720

Db 661 TATTTAACATTATTTATATGCGGAATATATTTTAGACTCATCAATCAATAAAGTATTTA 720

Qy 721 TAATAGCAACTTTTGTGTAATGAAATGAATATCTATTAATATATGATATTATTATAAT 780

Db 721 TAATAGCAACTTTTGTGTAATGAAATGAATATCTATTAATATATGATATTATTATAAT 780

Qy 781 CCTATATCCTGTGACTGTCTCACTTAATCCTTTGTTTCTGACTAATTAGGCAAGGCTAT 840

Db 781 CCTATATCCTGTGACTGTCTCACTTAATCCTTTGTTTCTGACTAATTAGGCAAGGCTAT 840

Qy 841 GTGATTACAGGCTTTATCTCAGGGGCCAACTAGGCAGCCAACTTAAGCAAGATCCCATG 900

Db 841 GTGATTACAGGCTTTATCTCAGGGGCCAACTAGGCAGCCAACTTAAGCAAGATCCCATG 900

Qy 901 GGTGTGTGTTTATTTCACTTGATGATACAAATGAACACTTATAAGTGAAGTACTATC 960

Db 901 GGTGTGTGTTTATTTCACTTGATGATACAAATGAACACTTATAAGTGAAGTACTATC 960

Qy 961 CAGTTACTGCCGTTTGAATAATATGCTGCAATCTGAGCCAGTCTTAATGCGATGCA 1020

Db 961 CAGTTACTGCCGTTTGAATAATATGCTGCAATCTGAGCCAGTCTTAATGCGATGCA 1020

Qy 1021 GACAGAACTTGAATGTGTGAGTCAACCTGATGAAACCATAGCATCTCAGGAGATTTTCA 1080

Db 1021 GACAGAACTTGAATGTGTGAGTCAACCTGATGAAACCATAGCATCTCAGGAGATTTTCA 1080

Qy 1081 GCCTGGTGTCTCCAAATATTTGTTGACAACTGTGACTGTACCCAAATGGAAGTAACTCAT 1140

Db 1081 GCCTGGTGTCTCCAAATATTTGTTGACAACTGTGACTGTACCCAAATGGAAGTAACTCAT 1140

Qy 1141 TTGTTAAAAATTATCAATATCTAATATATATATGAATAAAAGTGTAAGTTCACAACT 1193

Db 1141 TTGTTAAAAATTATCAATATCTAATATATATATGAATAAAAGTGTAAGTTCACAACT 1193

RESULT 2

US-10-641-643-1302

; Sequence 1302, Application US/10641643

; Publication No. US20040077003A1

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; Susan G. Stuart

; Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESS: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/641,643

; FILING DATE: 14-Aug-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: <Unknown>

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1302:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1193 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENBANK

; CLONE: g32691

; SEQUENCE DESCRIPTION: SEQ ID NO: 1302 :

US-10-641-643-1302

Query Match 100.0%; Score 1193; DB 16; Length 1193;

Best Local Similarity 100.0%; Pred. No. 2.6e-244;

Matches 1193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAAGATCAGCTATTAGAAGAGAAAGATCAGTTAAGTCCTTTGGACCTTGATCAGCTTGAT 60

Db 1 TGAAGATCAGCTATTAGAAGAGAAAGATCAGTTAAGTCCTTTGGACCTTGATCAGCTTGAT 60

Qy 61 ACAAGAACTACTGATTTCAACTCTTTGGCTTAATTTCTCTCGGAAACGATGAAATATACA 120

Db 61 ACAAGAACTACTGATTTCAACTCTTTGGCTTAATTTCTCTCGGAAACGATGAAATATACA 120

Qy 121 AGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTGGGTTCTCTTGGCTGTACTGCCAG 180

Db 121 AGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTGGGTTCTCTTGGCTGTACTGCCAG 180

Qy 181 GACCCATATGTAAGAAGCAGAAAAACCTTAAGAAATATTTTAATGCAGTCAATTCAGAT 240

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 26, 2004, 10:00:30 ; Search time 31.5556 Seconds
(without alignments)
1887.118 Million cell updates/sec

Title: US-10-655-873-12
Perfect score: 856
Sequence: 1 MKYTSYILAFQLCIVLGSGLG.....AKTGKRRSQMLFQGRRASQ 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	856	100.0	166	1	AAP93414
2	856	100.0	166	7	ADF76401
3	856	100.0	166	7	ADM13723
4	856	100.0	166	8	ADP12492
5	856	100.0	166	8	ADO19766
6	856	100.0	166	8	ADQ09094
7	852	99.5	166	1	AAP30093
8	852	99.5	166	1	AAP40122
9	852	99.5	166	1	AAP40153
10	852	99.5	166	1	AAP40157
11	852	99.5	166	1	AAP50233
12	852	99.5	166	2	AAW70582
13	852	99.5	166	4	AAE99130
14	852	99.5	166	5	AAE15823
15	852	99.5	166	5	AAU78100
16	852	99.5	166	5	AAU98670
17	852	99.5	166	5	ABB07440
18	852	99.5	166	6	ABR55848
19	852	99.5	166	6	ABR40017
20	852	99.5	166	6	ABP56461
21	852	99.5	166	6	ADA94887
22	852	99.5	166	7	ADC78909
23	852	99.5	166	8	ADG45031
24	852	99.5	166	8	ADJ56129
25	852	99.5	166	8	ADJ25952

26	852	99.5	166	8	ADM41333	Adm41333 Human int
27	852	99.5	166	8	ADN02800	Adn02800 Human int
28	852	99.5	166	8	ADN49692	Adn49692 Human int
29	848	99.1	166	1	AAP60250	Aap60250 Modified
30	848	99.1	166	1	AAP99990	Aap99990 Modified
31	847	98.9	166	1	AAP60090	Aap60090 Interfero
32	845	98.7	166	1	AAP50284	Aap50284 Human int
33	844	98.6	166	1	AAP30187	Aap30187 Sequence
34	843	98.5	166	1	AAP40255	Aap40255 Human imm
35	843	98.5	166	1	AAP40043	Aap40043 Sequence
36	842	98.4	166	1	AAP30002	Aap30002 Sequence
37	841	98.2	166	1	AAP40307	Aap40307 Sequence
38	826	96.5	166	1	AAP50170	Aap50170 Sequence
39	755	88.2	146	8	ADL88865	Adl88865 Human cyt
40	755	88.2	147	1	AAP60787	Aap60787 Sequence
41	755	88.2	147	1	AAP81208	Aap81208 Left and
42	755	88.2	177	1	AAP81210	Aap81210 Clal-BamH
43	751	87.7	146	1	AAP50128	Aap50128 Sequence
44	751	87.7	146	1	AAP60615	Aap60615 GFI146 ga
45	751	87.7	146	1	AAP60344	Aap60344 Human gam

ALIGNMENTS

RESULT 1
AAP93414
ID AAP93414 standard; protein; 166 AA.
XX
AC AAP93414;
XX
DT 27-APR-1990 (first entry)
XX
DE IFN211 , IFN-gamma mutant.
XX
KW Interferon-gamma; mutant; IFN211.
XX
OS Homo sapiens.
XX
PN EP343388-A.
XX
PD 29-NOV-1989.
XX
PF 25-APR-1989; 89EP-00107460.
XX
PR 25-APR-1988; 88US-00185219.
XX
PA (PHIP) PHILLIPS PETROLEUM CO.
XX
PI Thill GP, Davis GR;
XX
DR WPI; 1989-349507/48.
DR N-PSDB; AAN92425.
XX
PT Enhanced prodn. of interferon-gamma - using methylotrophic yeast, esp.
PT Pichia pastoris, transformed with linear integrative site-specific vector.
XX
PS Disclosure; Page 7; 26pp; English.
XX
CC IFN211 is a mutated form of IFN-gamma structural gene created by deleting the signal sequence by creating an EcoRI site and second start codon at approx. 66, 67, and 68 of the wt sequence. The mutant gene is used to construct IFN-gamma cytoplasmic expression vectors esp. methylotrophic yeast vectors for transfection of Pichia pastoris. See also AAP93416
XX
SQ Sequence 166 AA;

Query Match 100.0%; Score 856; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. NO. 2e-77;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKYTSYILAFQLCIVLGSGLGICYQDPYVKEAENLKKYFNAGHSDVADNGTFLGILKNWK 60

Db | 1 MKYTSYILAFQLCIVLGLGCGYQDPYVKEAENLKRYFNAGHSDVADNGTLFLGILKNWK 60
QY 61 EESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKGRDDFEKLTN 120
Db 61 EESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKGRDDFEKLTN 120
QY 121 YSVTDLNVQKAIHELIIQVMAELSPAAGTKGKRKRSQMLFQGRRASQ 166
Db 121 YSVTDLNVQKAIHELIIQVMAELSPAAGTKGKRKRSQMLFQGRRASQ 166

RESULT 2
ADF76401
ID ADF76401 standard; protein; 166 AA..
XX
AC ADF76401;
XX
DT 26-FEB-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein SeqID 74.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neurotrophin; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
PN WO2003072035-A2.
XX
PD 04-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US005241.
XX
PR 22-FEB-2002; 2002US-0359461P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
PI Williams PM, Wood WI, Wu TD;
XX
DR WPI; 2003-721702/68.
DR N-PSDB; ADF76400.

XX
PT New PRO polypeptides, useful for diagnosing and treating an immune
PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
PT diabetes mellitus.
XX
PS Claim 10; SEQ ID NO 74; 918pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neurotrophins and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is the amino acid sequence of a human PRO protein of the

CC invention.
XX
SQ Sequence 166 AA;
Query Match 100.0%; Score 856; DB 7; Length 166;
Best Local Similarity 100.0%; Pred. No. 2e-77;
Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKYTSYILAFQLCIVLGLGCGYQDPYVKEAENLKRYFNAGHSDVADNGTLFLGILKNWK 60
Db 1 MKYTSYILAFQLCIVLGLGCGYQDPYVKEAENLKRYFNAGHSDVADNGTLFLGILKNWK 60
QY 61 EESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKGRDDFEKLTN 120
Db 61 EESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKGRDDFEKLTN 120
QY 121 YSVTDLNVQKAIHELIIQVMAELSPAAGTKGKRKRSQMLFQGRRASQ 166
Db 121 YSVTDLNVQKAIHELIIQVMAELSPAAGTKGKRKRSQMLFQGRRASQ 166

RESULT 3
ADM13723
ID ADM13723 standard; protein; 166 AA.
XX
AC ADM13723;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human interferon-gamma protein.
XX
KW Interferon; IFN; Alzheimer's disease; Down syndrome; infant encephalitis;
KW autoimmune disease; HIV; AIDS-associated dementia; lupus erythematosus;
KW ulcerative colitis; Hashimoto's disease; amyotrophic lateral sclerosis;
KW Goodpasture's syndrome; therapy; acquired immunodeficiency syndrome;
KW AIDS; human.
XX
OS Homo sapiens.
XX
PN US2003138404-A1.
PD 24-JUL-2003.
XX
PF 31-OCT-2002; 2002US-00284740.
XX
PR 14-JUL-1995; 95US-00502519.
PR 28-APR-1998; 98US-00067398.
PR 30-APR-2001; 2001US-00845260.
XX
PA (MEIO-) MEIOGEN BIOTECHNOLOGY CORP.
XX
PI Maroun LE;
XX
DR WPI; 2003-829690/77.
DR N-PSDB; ADM13724.
DR GENBANK; X13274.
XX
PT Composition for preventing or decreasing pathological effects of disease
PT that are associated with increased level of or heightened responsiveness
PT to interferon, comprises at least two isolated interferon binding
PT proteins.
XX
PS Disclosure; Fig 7B; 38pp; English.
XX
CC The present invention provides composition for preventing or decreasing
CC pathological effects of a disease that are associated with an increased
CC level of or a heightened responsiveness to interferon (IFN) where the
CC composition inhibits the activity of one or more IFN. The invention is
CC useful for treating diseases such as Alzheimer's disease, Down syndrome,
CC infant encephalitis, autoimmune diseases such as lupus erythematosus,
CC ulcerative colitis, Hashimoto's disease, amyotrophic lateral sclerosis
CC and Goodpasture's syndrome and HIV where the administration of the
CC antagonist prevents or ameliorates AIDS (acquired immunodeficiency